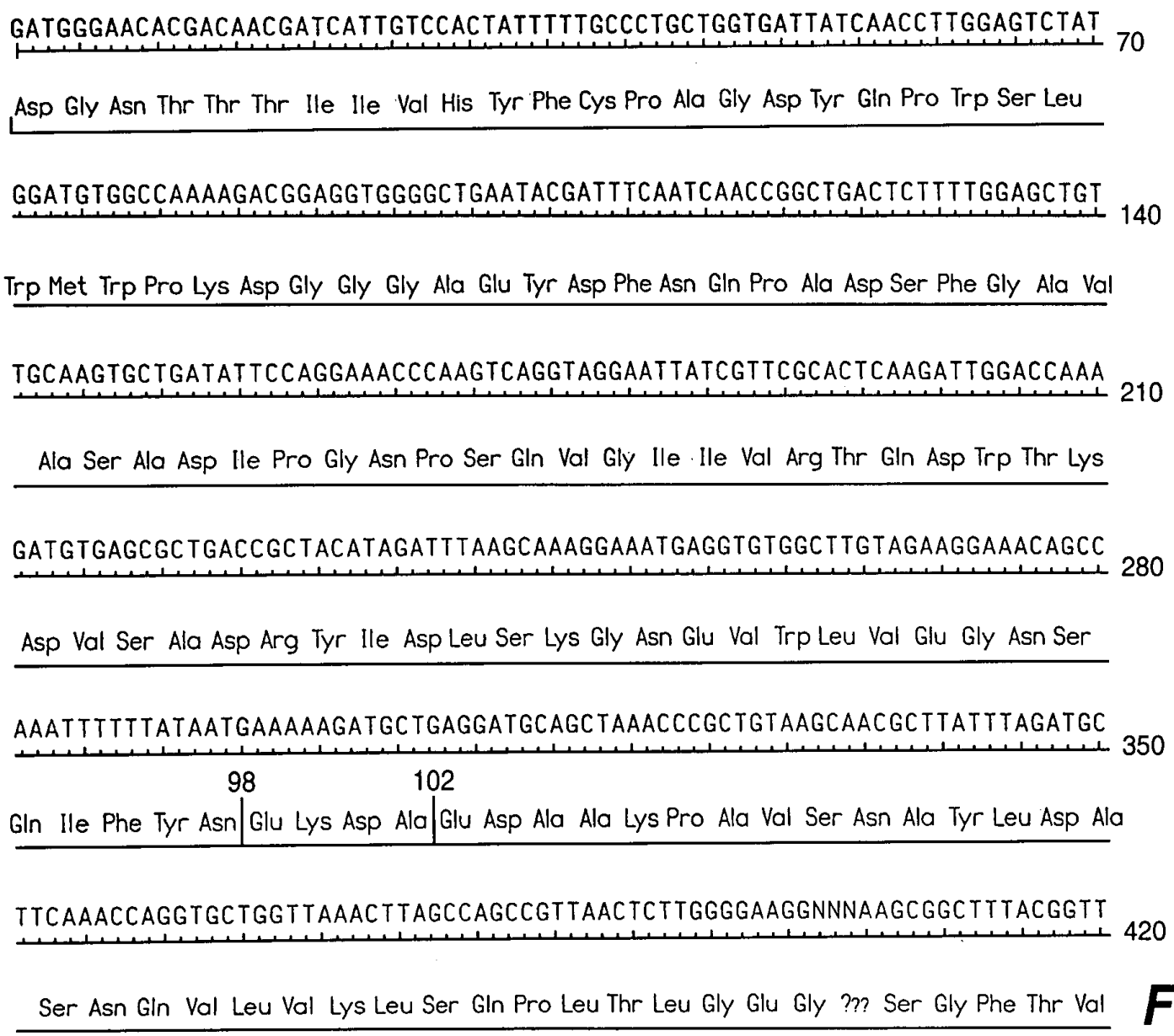
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GGATGTGGCCAAAAGACGGAGGTGGGGCTGAATACGATTTCAATCAACCGGCTGACTCTTTTGGAGCTGT 140
Trp Met Trp Pro Lys Asp Gly Gly Gly Ala Glu Tyr Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val
TGCAAGTGCTGATATTCCAGGAAACCCAAGTCAGGTAGGAATTATCGTTCGCACTCAAGATTGGACCAAA 210
Ala Ser Ala Asp Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg Thr Gln Asp Trp Thr Lys
GATGTGAGCGCTGACCGCTACATAGATTTAAGCAAAGGAAATGAGGTGTGGCTTGTAGAAGGAAACAGCC 280
Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu Ser Lys Gly Asn Glu Val Trp Leu Val Glu Gly Asn Ser
AAATTTTTTATAATGAAAAAGATGCTGAGGATGCAGCTAAACCCGCTGTAAGCAACGCTTATTTAGATGC 350
98 102
Gln Ile Phe Tyr Asn Glu Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn Ala Tyr Leu Asp Ala
TTCAAACCAGGTGCTGGTTAAACTTAGCCAGCCGTTAACTCTTGGGGAAGGNNNAAGCGGCTTTACGGTT 420
Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro Leu Thr Leu Gly Glu Gly ??? Ser Gly Phe Thr Val

FIG._1A

```
CATGACGACACAGCAAATAAGGATATTCCAGTGACATCTGTGAAGGATGCAAGTCTTGGTCAAGATGTAA                490
 His Asp Asp Thr Ala Asn Lys Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly Gln Asp Val

CCGCTGTTTTGGCAGGTACCTTCCAACATATTTTTGGAGGTTCCGATTGGGCACCTGATAATCACAGTAC              560
Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly Gly Ser Asp Trp Ala Pro Asp Asn His Ser Thr

TTTATTAAAAAAGGTGACTAACAATCTCTATCAATTCTCAGGAGATCTTCCTGAAGGAAACTACCAATAT              630
 Leu Leu Lys Lys Val Thr Asn Asn Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr

AAAGTGGCTTTAAATGATAGCTGGAATAATCCGAGTTACCCATCTGACAACATTAATTTAACAGTCCCTG              700
 Lys Val Ala Leu Asn Asp Ser Trp Asn Asn Pro Ser Tyr Pro Ser Asp Asn Ile Asn Leu Thr Val Pro

CCGGCGGTGCACACGTCACTTTTTCGTATATTCCGTCCACTCATGCAGTCTATGACACAATTAATAATCC              770
Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro

TAATGCGGATTTACAAGTAGAAAGCGGGGTTAAAACGGATCTCGTGACGGTTACTCTAGGGGAAGATCCA              840
 Asn Ala Asp Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu Gly Glu Asp Pro
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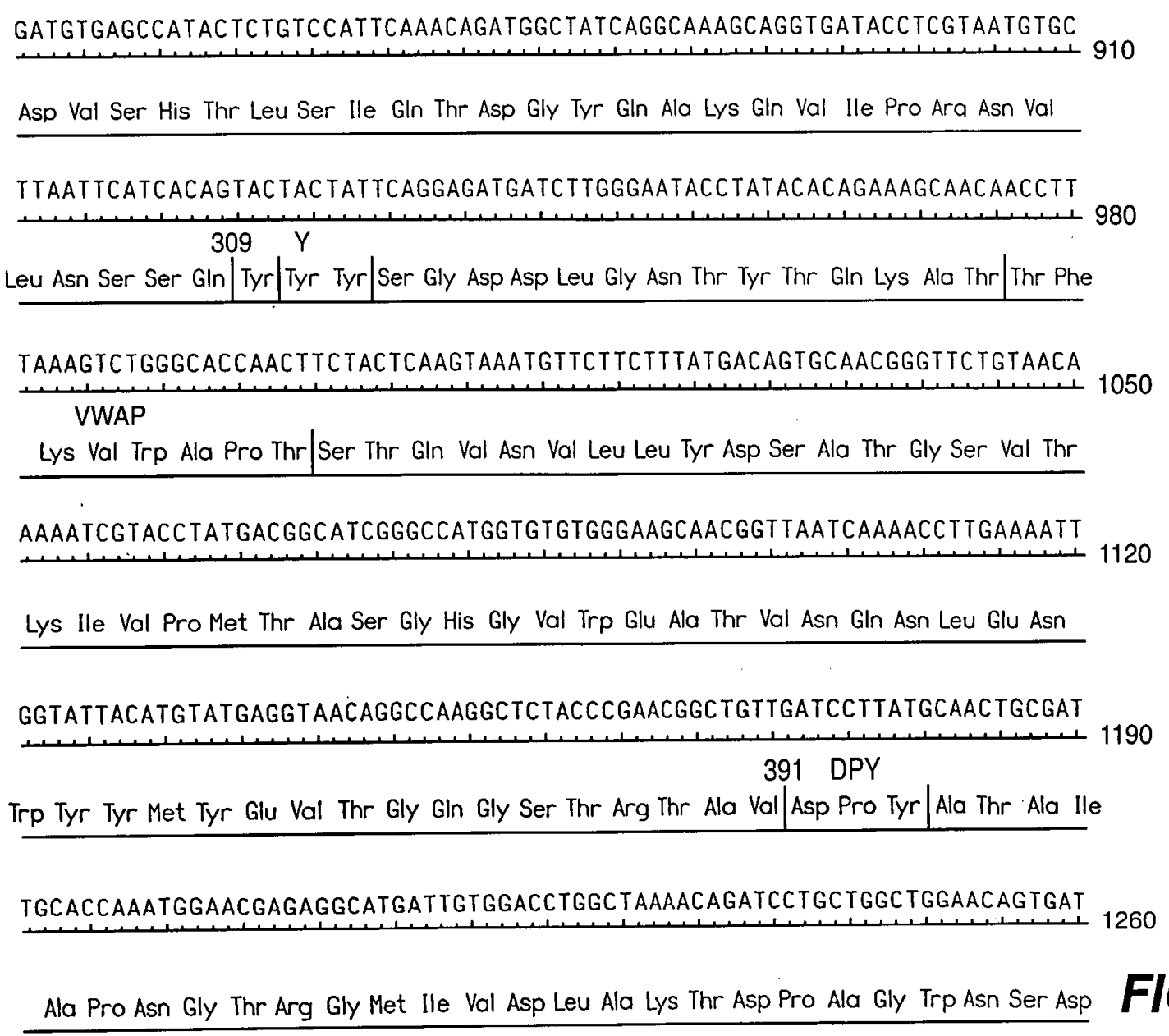
FIG._1B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910
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TTAATTCATCACAGTACTACTATTCAGGAGATGATCTTGGGAATACCTATACACAGAAAGCAACAACCTT
980
309 Y
Leu Asn Ser Ser Gln Tyr Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala Thr Thr Phe
TAAAGTCTGGGCACCAACTTCTACTCAAGTAAATGTTCTTCTTTATGACAGTGCAACGGGTTCTGTAACA
1050
VWAP
Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr
AAAATCGTACCTATGACGGCATCGGGCCATGGTGTGTGGGAAGCAACGGTTAATCAAAACCTTGAAAATT
1120
Lys Ile Val Pro Met Thr Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu Asn
GGTATTACATGTATGAGGTAACAGGCCAAGGCTCTACCCGAACGGCTGTTGATCCTTATGCAACTGCGAT
1190
391 DPY
Trp Tyr Tyr Met Tyr Glu Val Thr Gly Gln Gly Ser Thr Arg Thr Ala Val Asp Pro Tyr Ala Thr Ala Ile
TGCACCAAATGGAACGAGAGGCATGATTGTGGACCTGGCTAAAACAGATCCTGCTGGCTGGAACAGTGAT
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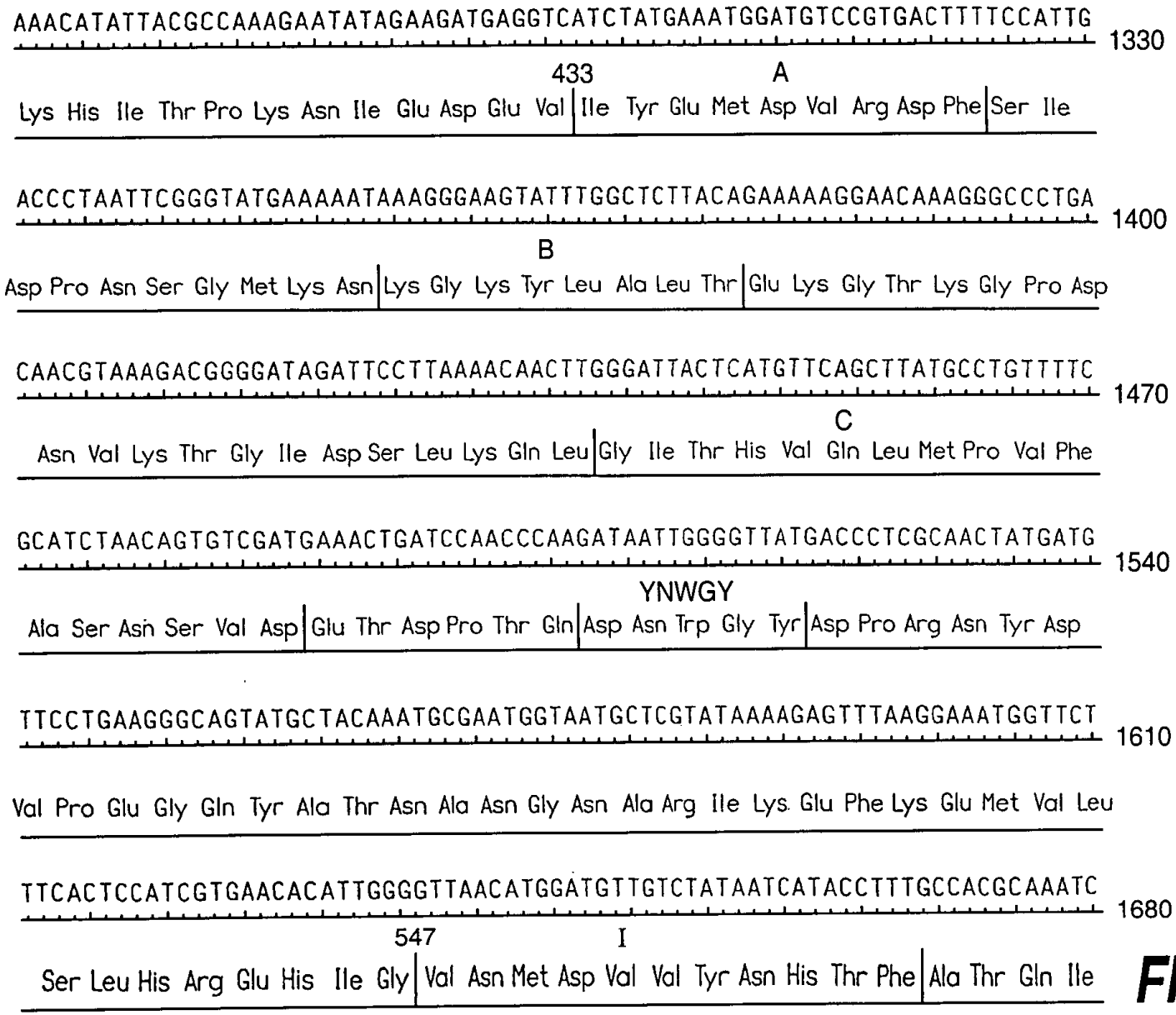
FIG._1C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1330
433
A
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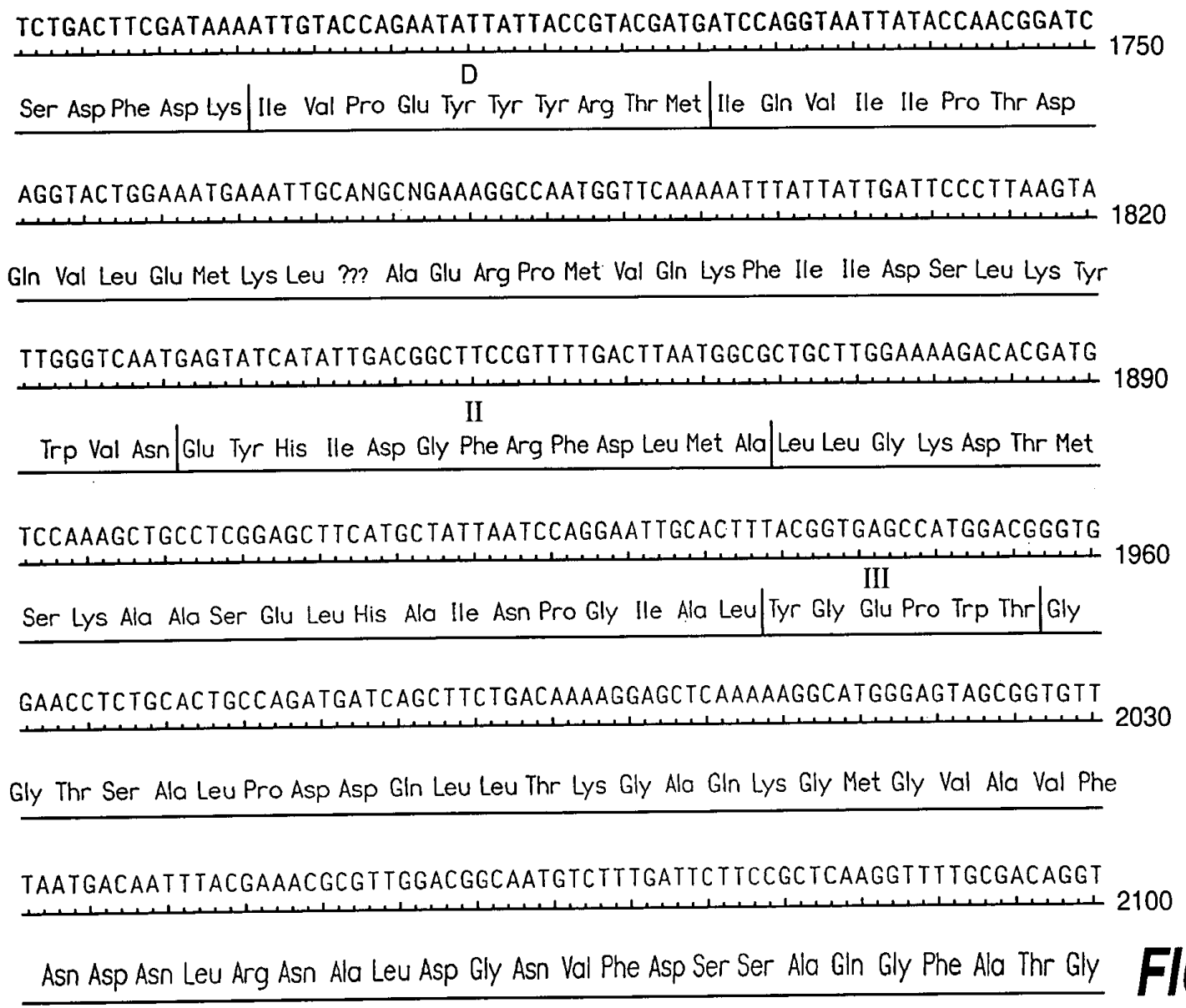
ACCCTAATTCGGGTATGAAAAATAAAGGGAAGTATTTGGCTCTTACAGAAAAAGGAACAAAGGGCCCTGA
1400
B
Asp Pro Asn Ser Gly Met Lys Asn | Lys Gly Lys Tyr Leu Ala Leu Thr | Glu Lys Gly Thr Lys Gly Pro Asp
CAACGTAAAGACGGGGATAGATTCCTTAAAACAACTTGGGATTACTCATGTTCAGCTTATGCCTGTTTTC
1470
C
Asn Val Lys Thr Gly Ile Asp Ser Leu Lys Gln Leu | Gly Ile Thr His Val Gln Leu Met Pro Val Phe
GCATCTAACAGTGTCGATGAAACTGATCCAACCCAAGATAATTGGGGTTATGACCCTCGCAACTATGATG
1540
YNWGY
Ala Ser Asn Ser Val Asp | Glu Thr Asp Pro Thr Gln | Asp Asn Trp Gly Tyr | Asp Pro Arg Asn Tyr Asp
TTCCTGAAGGGCAGTATGCTACAAATGCGAATGGTAATGCTCGTATAAAAGAGTTTAAGGAAATGGTTCT
1610
Val Pro Glu Gly Gln Tyr Ala Thr Asn Ala Asn Gly Asn Ala Arg Ile Lys Glu Phe Lys Glu Met Val Leu
TTCACTCCATCGTGAACACATTGGGGTTAACATGGATGTTGTCTATAATCATACCTTTGCCACGCAAATC
1680
547
I
Ser Leu His Arg Glu His Ile Gly | Val Asn Met Asp Val Val Tyr Asn His Thr Phe | Ala Thr Gln Ile

FIG._1D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1750
D
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AGGTACTGGAAATGAAATTGCANGCNGAAAGGCCAATGGTTCAAAAATTTATTATTGATTCCCTTAAGTA
1820
Gln Val Leu Glu Met Lys Leu ??? Ala Glu Arg Pro Met Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr
TTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTTGACTTAATGGCGCTGCTTGGAAAAGACACGATG
1890
II
Trp Val Asn | Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala | Leu Leu Gly Lys Asp Thr Met
TCCAAAGCTGCCTCGGAGCTTCATGCTATTAATCCAGGAATTGCACTTTACGGTGAGCCATGGACGGGTG
1960
III
Ser Lys Ala Ala Ser Glu Leu His Ala Ile Asn Pro Gly Ile Ala Leu | Tyr Gly Glu Pro Trp Thr | Gly
GAACCTCTGCACTGCCAGATGATCAGCTTCTGACAAAAGGAGCTCAAAAAGGCATGGGAGTAGCGGTGTT
2030
Gly Thr Ser Ala Leu Pro Asp Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val Phe
TAATGACAATTTACGAAACGCGTTGGACGGCAATGTCTTTGATTCTTCCGCTCAAGGTTTTGCGACAGGT
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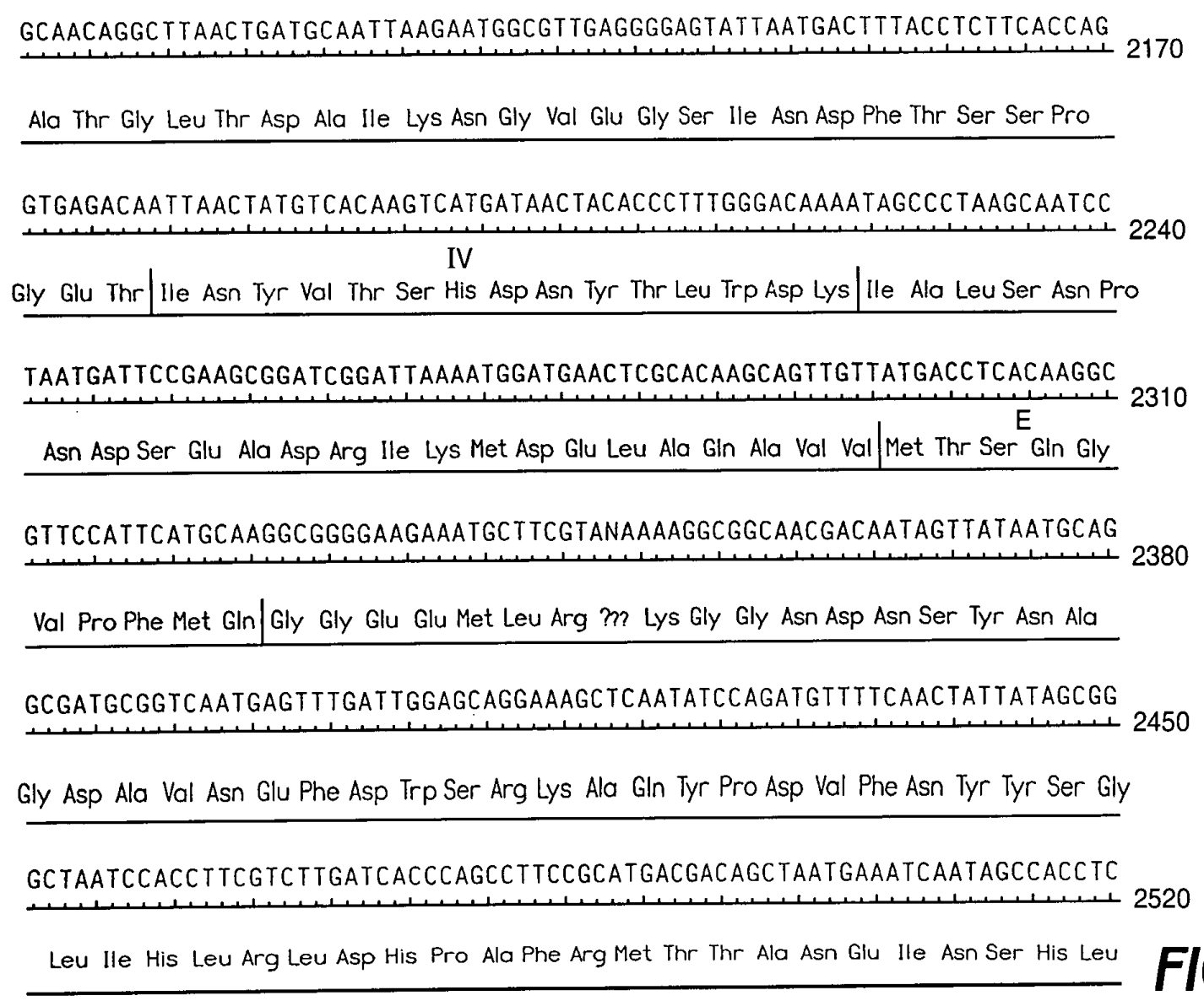
FIG._1E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2170
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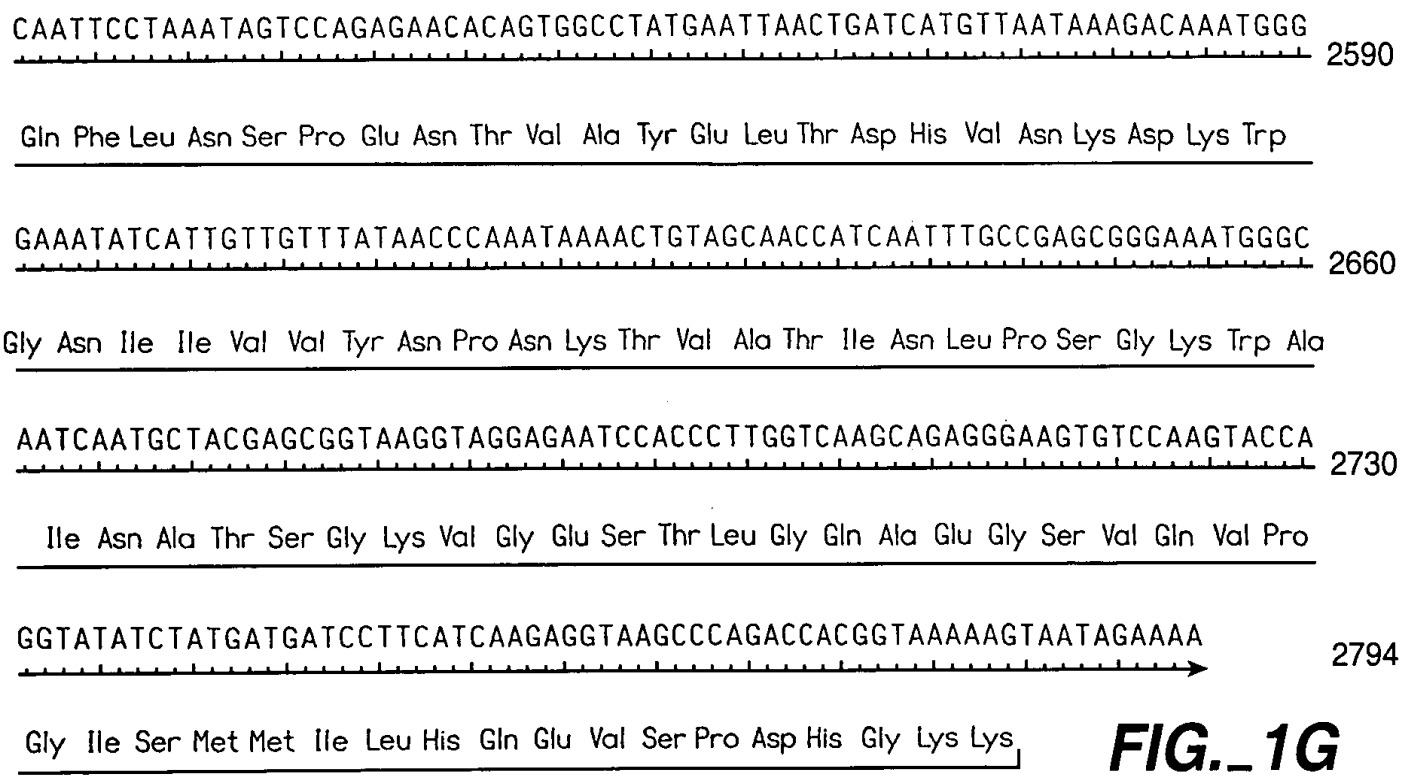
GTGAGACAATTAACTATGTCACAAGTCATGATAACTACACCCTTTGGGACAAAATAGCCCTAAGCAATCC
2240
IV
Gly Glu Thr | Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp Lys | Ile Ala Leu Ser Asn Pro
TAATGATTCCGAAGCGGATCGGATTAAAATGGATGAACTCGCACAAGCAGTTGTTATGACCTCACAAGGC
2310
E
Asn Asp Ser Glu Ala Asp Arg Ile Lys Met Asp Glu Leu Ala Gln Ala Val Val | Met Thr Ser Gln Gly
GTTCCATTCATGCAAGGCGGGGAAGAAATGCTTCGTANAAAAGGCGGCAACGACAATAGTTATAATGCAG
2380
Val Pro Phe Met Gln | Gly Gly Glu Glu Met Leu Arg ??? Lys Gly Gly Asn Asp Asn Ser Tyr Asn Ala
GCGATGCGGTCAATGAGTTTGATTGGAGCAGGAAAGCTCAATATCCAGATGTTTTCAACTATTATAGCGG
2450
Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly
GCTAATCCACCTTCGTCTTGATCACCCAGCCTTCCGCATGACGACAGCTAATGAAATCAATAGCCACCTC
2520
Leu Ile His Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile Asn Ser His Leu

FIG._1F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GAAATATCATTGTTGTTTATAACCCAAATAAAACTGTAGCAACCATCAATTTGCCGAGCGGGAAATGGGC
2660
Gly Asn Ile Ile Val Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly Lys Trp Ala
AATCAATGCTACGAGCGGTAAGGTAGGAGAATCCACCCTTGGTCAAGCAGAGGGAAGTGTCCAAGTACCA
2730
Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu Gly Gln Ala Glu Gly Ser Val Gln Val Pro
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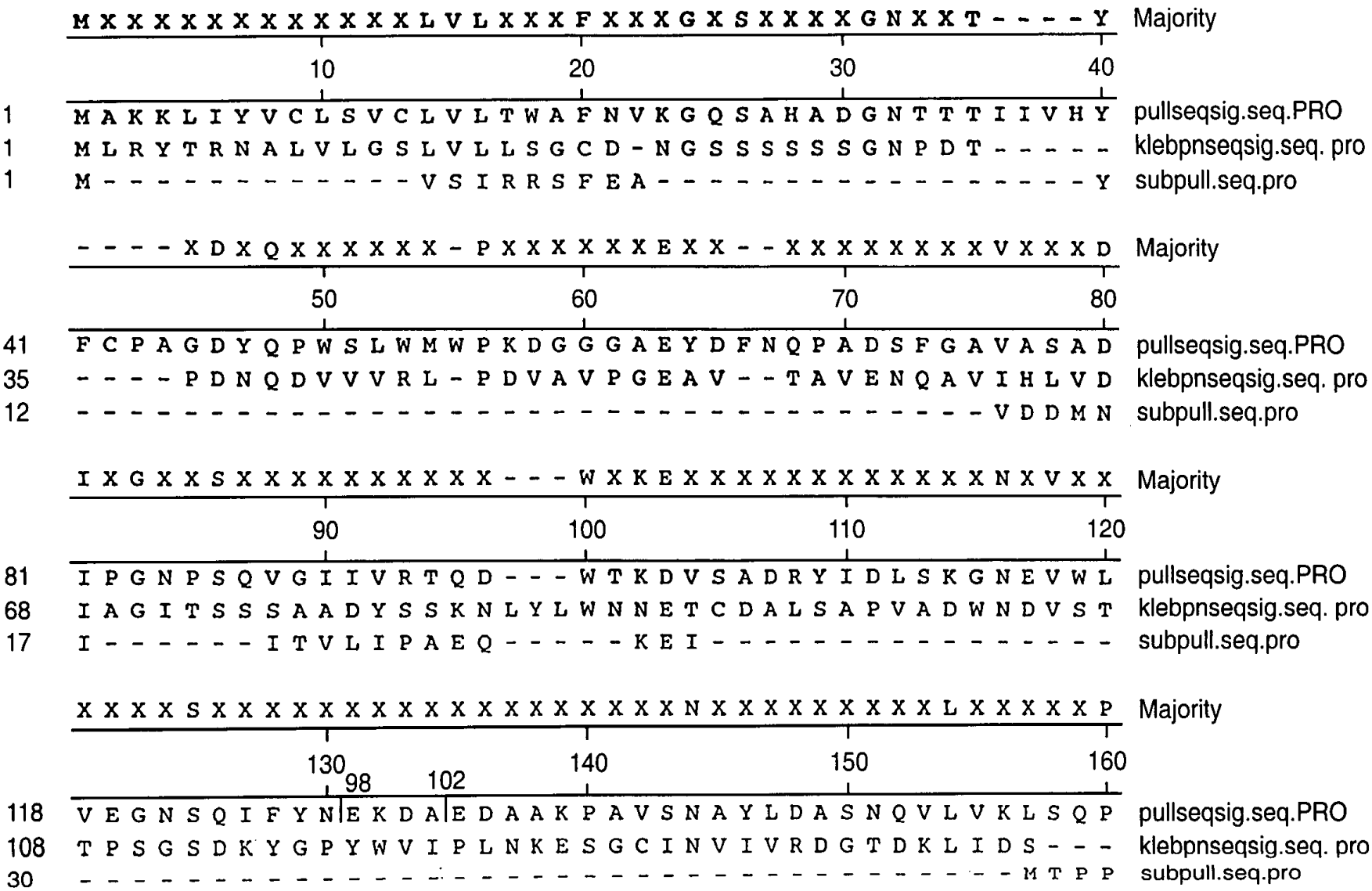
2794
Gly Ile Ser Met Met Ile Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys

FIG._1G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1 MLRYTRNALVLGSLVLLSGCD-NGSSSSSSGNPDT----- klebpnseqsig.seq. pro
1 M----------VSIRRSFEA----------------Y subpull.seq.pro
----XDXQXXXXX-PXXXXXXEXX--XXXXXXXXVXXXD Majority
50 60 70 80
41 FCPAGDYQPWSLWMWPKDGGGAEYDFNQPADSFGAVASAD pullseqsig.seq.PRO
35 ----PDNQDVVVRL-PDVAVPGEAV--TAVENQAVIHLVD klebpnseqsig.seq. pro
12 ----------------------------VDDMN subpull.seq.pro
IXGXXSXXXXXXXXX---WXKEXXXXXXXXXXXXNXVXX Majority
90 100 110 120
81 IPGNPSQVGIIVRTQD---WTKDVSADRYIDLSKGNEVWL pullseqsig.seq.PRO
68 IAGITSSSAADYSSKNLYLWNNETCDALSAPVADWNDVST klebpnseqsig.seq. pro
17 I-------ITVLIPAEQ-----KEI---------------- subpull.seq.pro
XXXXSXXXXXXXXXXXXXXXXXXNXXXXXXXXLXXXXP Majority
130 140 150 160
98 102
118 VEGNSQIFYNEKDAEDAAKPAVSNAYLDASNQVLVKLSQP pullseqsig.seq.PRO
108 TPSGSDKYGPYWVIPLNKESGCINVIVRDGTDKLIDS--- klebpnseqsig.seq. pro
30 ----------------------------MTPP subpull.seq.pro

FIG._2A

```
     X X L X X X X X D F T - - - - - - X X X X P V X X X X X X S L X X X X X X X X X   Majority
                    170                 180                 190                 200
158  L T L G E G X S G F T V H D D T A N K D I P V T S V K D A S L G Q D V T A V L A   pullseqsig.seq.PRO
145  - D L R V A F G D F T - - - - - - D R T V S V - I A G N S A V Y D S R A D A F R   klebpnseqsig.seq. pro
34   F R L E T E I T D F - - - - - - - - - - - - P L A V R E E Y S L - - - - - - - -   subpull.seq.pro

     X X F X X X X X X X W X - - X X X T L L - - - - - X K X X X X L Y - - - - - - -   Majority
                    210                 220                 230                 240
198  G T F Q H I F G G S D W A P D N H S T L L - - - - - K K V T N N L Y Q F S G D L   pullseqsig.seq.PRO
177  A A F G V A L A E A H W V - - D K N T L L W P G G Q D K P I V R L Y - - - - - -   klebpnseqsig.seq. pro
54   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   subpull.seq.pro

     - E X X Y X Y X X X X X X - X X X X X X X X X X L T V X X X X X V T F X X   Majority
                    250                 260                 270                 280
233  P E G N Y Q Y K V A L N D S W N N P S Y P S D N I N L T V P A G G A H V T F S Y   pullseqsig.seq.PRO
209  - - - - Y S H S S K V A A D - G E G K F T D R Y L K L T P T T V S Q Q V S M R F   klebpnseqsig.seq. pro
54   - E A K Y K Y - - - - - - - - - - - - - - - - - - - - - V C V S D H P V T F G K   subpull.seq.pro

     I H X X X A X Y X X X X X P X - X X X V X S G X K T D L V X X A X X E D X X X X   Majority
                    290                 300                 310                 320
273  I P S T H A V Y D T I N N P N A D L Q V E S G V K T D L V T V T L G E D P D V S   pullseqsig.seq.PRO
244  P H - - L S S Y A A F K L P D - N A N V D E L L Q G E T V A I A A A E D G I L I   klebpnseqsig.seq. pro
72   I H C V R A - - - - - - - - - - - - - - - - S S G H K T D L Q I G A V - - - - - -   subpull.seq.pro
```

FIG._2B

```
    XXXXIQTAGXXX  ------VLXXXXYYYXGEXL--GAXYT  Majority
                330       340      Y 350       360
313 HTLSIQTDGYQAKQVIPRNVLNSSQYYY|SGDDL--GNTYT  pullseqsig.seq.PRO
281 SATQVQTAG----------VLDDA-Y|AE|AAEALSYGAQLA  klebpnseqsig.seq. pro
91  ----IRTAAFDD----------EF|YY|DGE-L--GAVYT  subpull.seq.pro

    XXXTTFKVWAPTATQVXVXLYXXXKXXXXXXXXMTXSXXG  Majority
          VWAP 370       380       390       400
351 QKAT|TFKVWAPT|STQVNVLLYDSATGSVTKIVPMTASGHG  pullseqsig.seq.PRO
310 DGGV|TFRVWAPT|AQQVDVVVYSADKKVIGSHPMTRDSASG  klebpnseqsig.seq. pro
112 ADHT|VFKVWAPA|ATSAAVKLSHPNKSG--RTFQMTRLEKG  subpull.seq.pro

    VWXXTVXXDLXGXXYXYXXTX-XXXXR-----EXVDPYAX  Majority
                410       420       430   DPY 440
391 VWEATVNQNLENWYYMYEVTG-QGSTR-----TAV|DPY|AT  pullseqsig.seq.PRO
350 AWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVT|DPY|AH  klebpnseqsig.seq. pro
150 VYAVTVTGDLHGYEYLFCICN-NSEWM-----ETV|DQY|AK  subpull.seq.pro

    AXXXNGEXGXVVDLXXXD--PXGWXXXXXPXXXXXXDXV-  Majority
                450       460       470       480
425 AIAPNGTRGMIVDLAKTD--PAGWNSDKHITPKNIEDEV-  pullseqsig.seq.PRO
390 SLSTNSEYSQVVDLNDSALKPDGWDNLTMPHAQKTKADLA  klebpnseqsig.seq. pro
184 AVTVNGEKGVVL---RPD--QMKWTAPLKPFSHPV-DAV-  subpull.seq.pro
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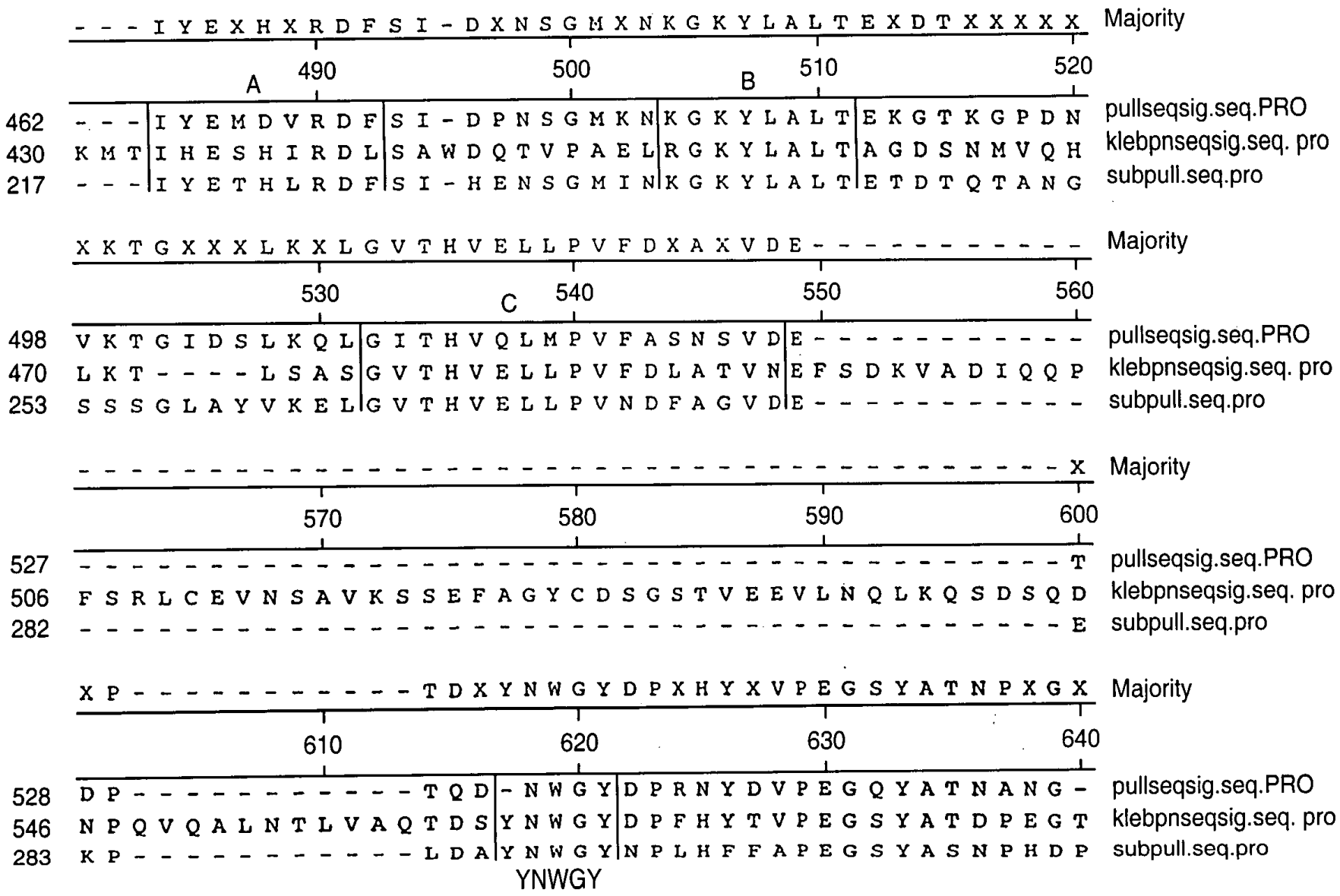
FIG._2C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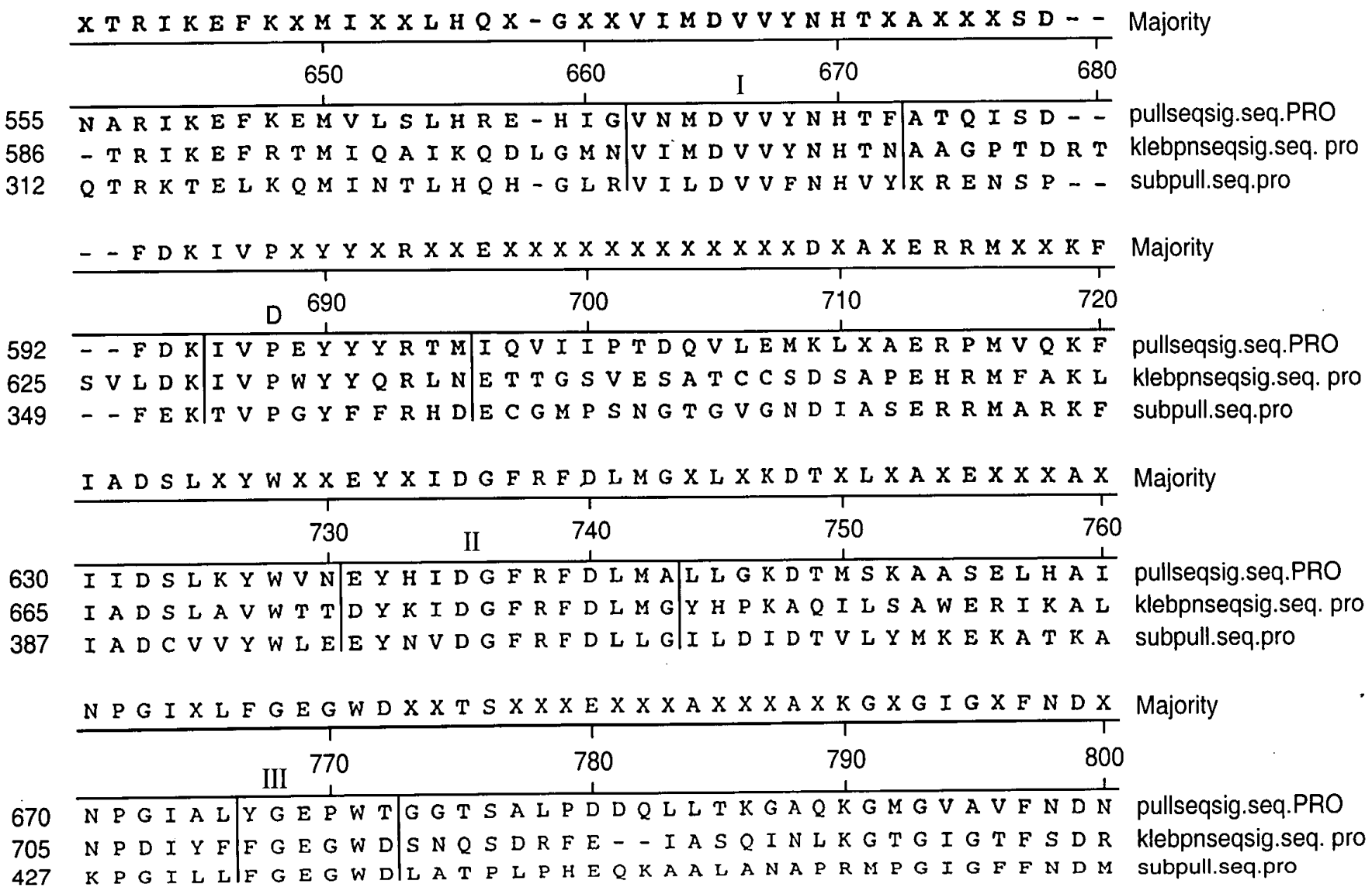
A
490
500
B
510
520
462 - - - I Y E M D V R D F S I - D P N S G M K N K G K Y L A L T E K G T K G P D N pullseqsig.seq.PRO
430 K M T I H E S H I R D L S A W D Q T V P A E L R G K Y L A L T A G D S N M V Q H klebpnseqsig.seq. pro
217 - - - I Y E T H L R D F S I - H E N S G M I N K G K Y L A L T E T D T Q T A N G subpull.seq.pro
X K T G X X X L K X L G V T H V E L L P V F D X A X V D E - - - - - - - - - - - - Majority
530
C
540
550
560
498 V K T G I D S L K Q L G I T H V Q L M P V F A S N S V D E - - - - - - - - - - - - pullseqsig.seq.PRO
470 L K T - - - - L S A S G V T H V E L L P V F D L A T V N E F S D K V A D I Q Q P klebpnseqsig.seq. pro
253 S S S G L A Y V K E L G V T H V E L L P V N D F A G V D E - - - - - - - - - - - - subpull.seq.pro
- X Majority
570
580
590
600
527 - T pullseqsig.seq.PRO
506 F S R L C E V N S A V K S S E F A G Y C D S G S T V E E V L N Q L K Q S D S Q D klebpnseqsig.seq. pro
282 - E subpull.seq.pro
X P - - - - - - - - - - - - T D X Y N W G Y D P X H Y X V P E G S Y A T N P X G X Majority
610
620
630
640
528 D P - - - - - - - - - - - - T Q D - N W G Y D P R N Y D V P E G Q Y A T N A N G - pullseqsig.seq.PRO
546 N P Q V Q A L N T L V A Q T D S Y N W G Y D P F H Y T V P E G S Y A T D P E G T klebpnseqsig.seq. pro
283 K P - - - - - - - - - - - - L D A Y N W G Y N P L H F F A P E G S Y A S N P H D P subpull.seq.pro
YNWGY

FIG._2D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Majority
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660
I
670
680
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586 -TRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRT klebpnseqsig.seq. pro
312 QTRKTELKQMINTLHQH-GLRVILDVVFNHVYKRENSP-- subpull.seq.pro
--FDKIVPXYYXRXXEXXXXXXXXXXXXXDXAXERRMXXKF
Majority
D
690
700
710
720
592 --FDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKF pullseqsig.seq.PRO
625 SVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKL klebpnseqsig.seq. pro
349 --FEKTVPGYFFRHDECGMPSNGTGVGNDIASERRMARKF subpull.seq.pro
IADSLXYWXXEYXIDGFRFDLMGXLXKDTXLXAXEXXXAX
Majority
730
II
740
750
760
630 IIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAI pullseqsig.seq.PRO
665 IADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKAL klebpnseqsig.seq. pro
387 IADCVVYWLEEYNVDGFRFDLLGILDIDTVLYMKEKATKA subpull.seq.pro
NPGIXLFGEGWDXXTSXXXEXXXAXXXAXKGXGIGXFNDX
Majority
III
770
780
790
800
670 NPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDN pullseqsig.seq.PRO
705 NPDIYFFGEGWDSNQSDRFE--IASQINLKGTGIGTFSDR klebpnseqsig.seq. pro
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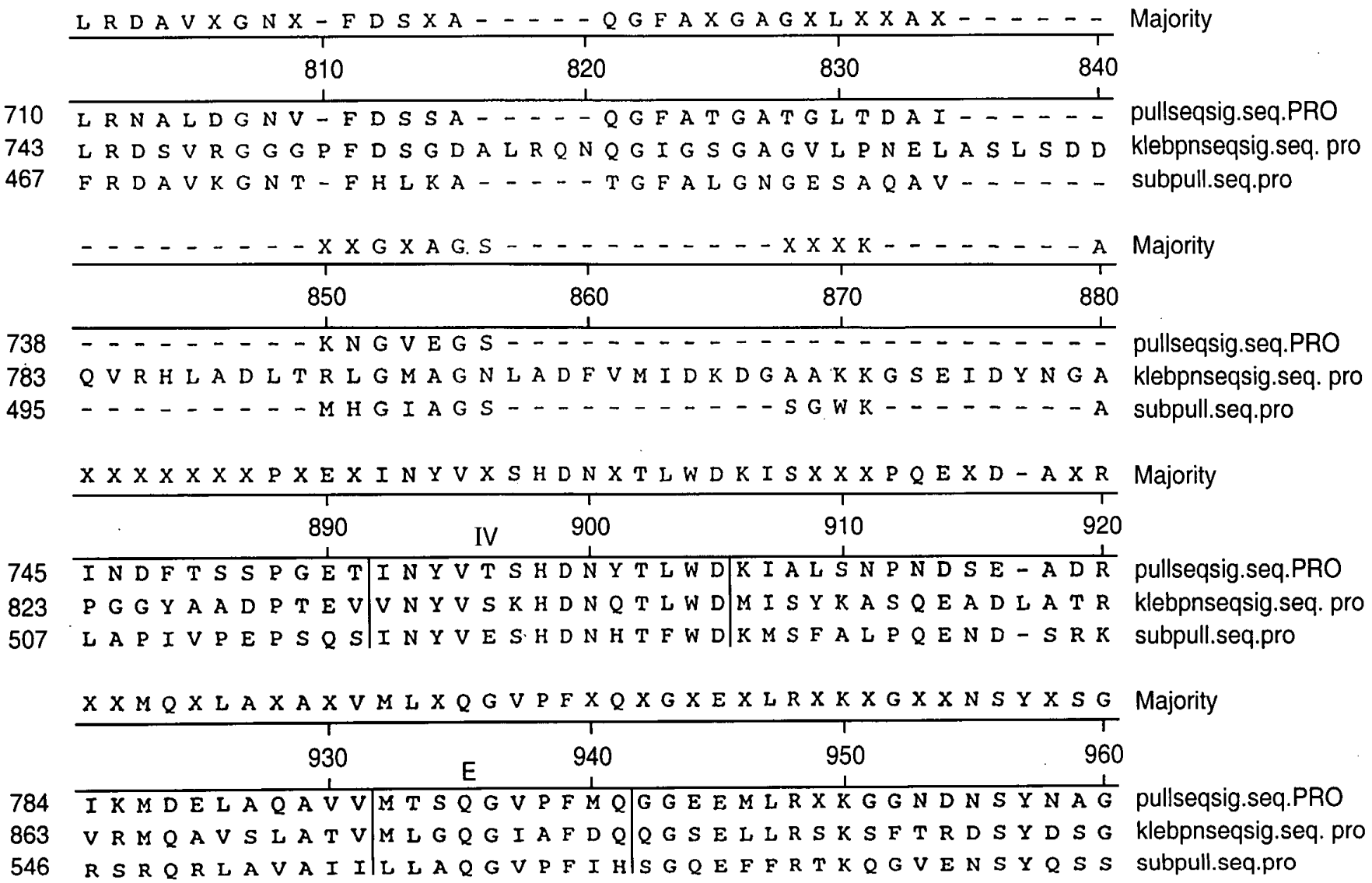
FIG._2E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710 LRNALDGNV-FDSSA-----QGFATGATGLTDAI------ pullseqsig.seq.PRO
743 LRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDD klebpnseqsig.seq. pro
467 FRDAVKGNT-FHLKA-----TGFALGNGESAQAV------ subpull.seq.pro
----------XXGXAG.S----------XXXK---------A Majority
850 860 870 880
738 ----------KNGVEGS---------- pullseqsig.seq.PRO
783 QVRHLADLTRLGMAGNLADFVMIDKDGAAKKGSEIDYNGA klebpnseqsig.seq. pro
495 ----------MHGIAGS----------SGWK---------A subpull.seq.pro
XXXXXXXPXEXINYVXSHDNXTLWDKISXXXPQEXD-AXR Majority
890 IV 900 910 920
745 INDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSE-ADR pullseqsig.seq.PRO
823 PGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATR klebpnseqsig.seq. pro
507 LAPIVPEPSQSINYVESHDNHTFWDKMSFALPQEND-SRK subpull.seq.pro
XXMQXLAXAXVMLXQGVPFXQXGXEXLRXKXGXXNSYXSG Majority
930 E 940 950 960
784 IKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAG pullseqsig.seq.PRO
863 VRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSG klebpnseqsig.seq. pro
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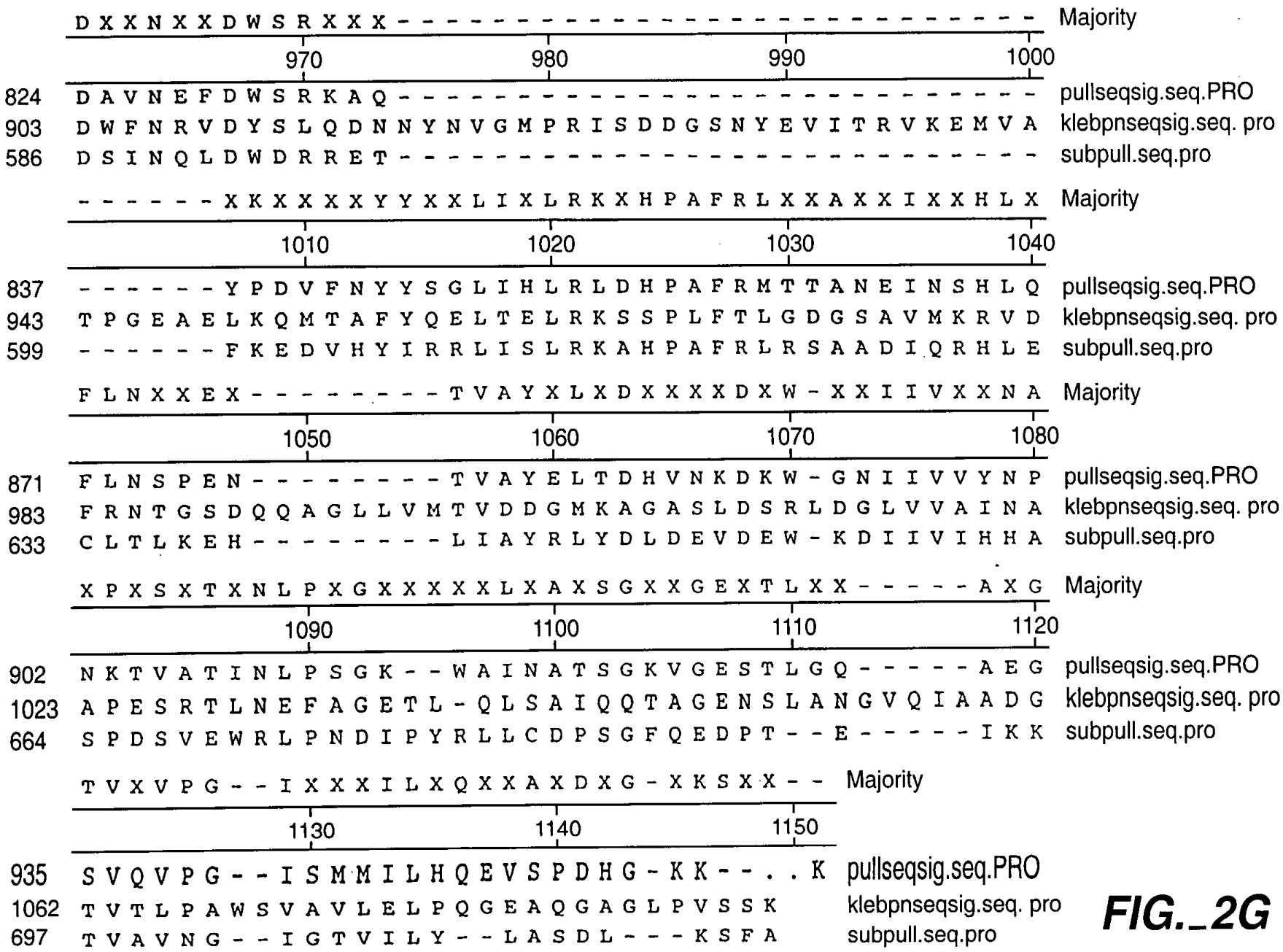
FIG._2F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586 DSINQLDWDRRET---------- subpull.seq.pro
------XKXXXXYYXXLIXLRKXHPAFRLXXAXXIXXHLX Majority
1010 1020 1030 1040
837 ------YPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQ pullseqsig.seq.PRO
943 TPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVD klebpnseqsig.seq. pro
599 ------FKEDVHYIRRLISLRKAHPAFRLRSAADIQRHLE subpull.seq.pro
FLNXXEX---------TVAYXLXDXXXXDXW-XXIIVXXNA Majority
1050 1060 1070 1080
871 FLNSPEN---------TVAYELTDHVNKDKW-GNIIVVYNP pullseqsig.seq.PRO
983 FRNTGSDQQAGLLVMTVDDGMKAGASLDSRLDGLVVAINA klebpnseqsig.seq. pro
633 CLTLKEH---------LIAYRLYDLDEVDEW-KDIIVIHHA subpull.seq.pro
XPXSXTXNLPXGXXXXXLXAXSGXXGEXTLXX-----AXG Majority
1090 1100 1110 1120
902 NKTVATINLPSGK--WAINATSGKVGESTLGQ-----AEG pullseqsig.seq.PRO
1023 APESRTLNEFAGETL-QLSAIQQTAGENSLANGVQIAADG klebpnseqsig.seq. pro
664 SPDSVEWRLPNDIPYRLLCDPSGFQEDPT--E-----IKK subpull.seq.pro
TVXVPG--IXXXILXQXXAXDXG-XKSXX-- Majority
1130 1140 1150
935 SVQVPG--ISMMILHQEVSPDHG-KK--..K pullseqsig.seq.PRO
1062 TVTLPAWSVAVLELPQGEAQGAGLPVSSK klebpnseqsig.seq. pro
697 TVAVNG--IGTVILY--LASDL---KSFA subpull.seq.pro

FIG._2G

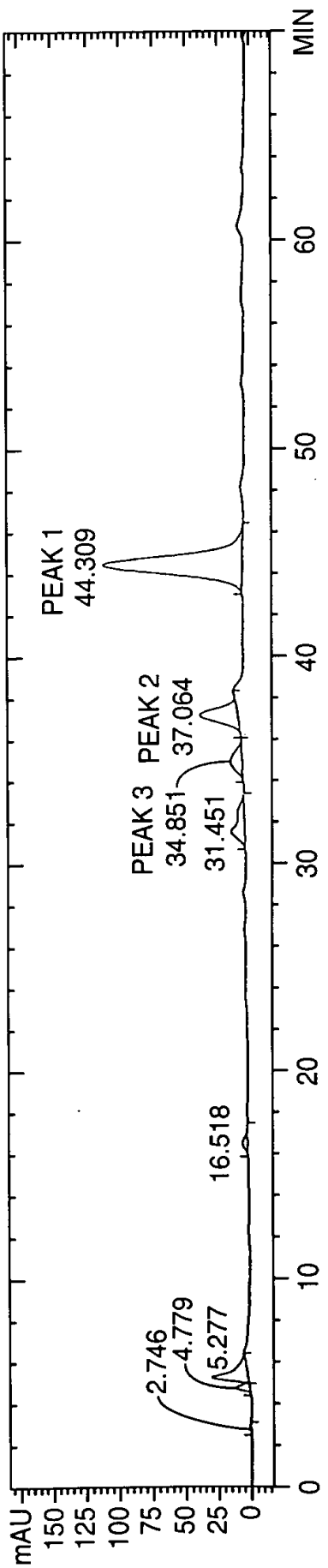
mAU
150
125
100
75
50
25
0
0
10
20
30
40
50
60
MIN
PEAK 1
44.309
PEAK 2
37.064
PEAK 3
34.851
31.451
16.518
2.746
4.779
5.277

FIG._3A

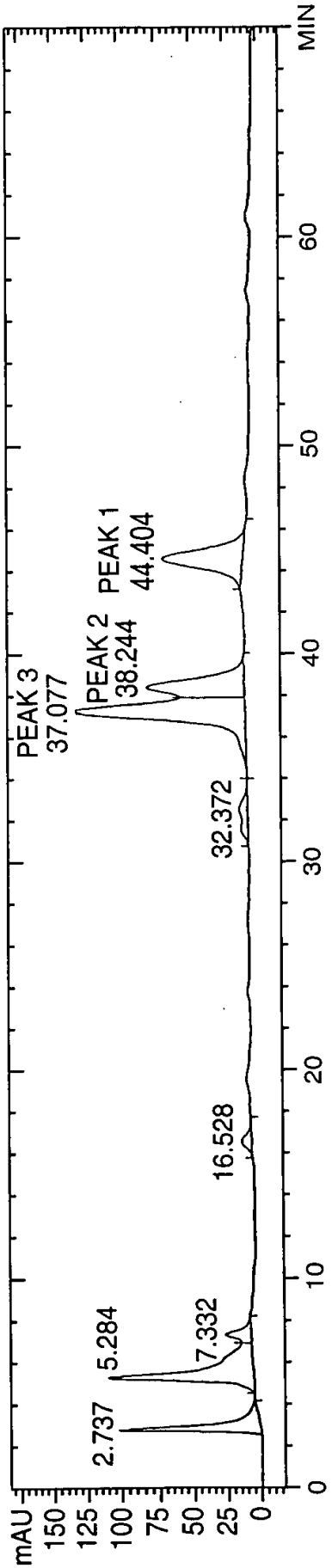
mAU
150
125
100
75
50
25
0
0
10
20
30
40
50
60
MIN
PEAK 1
44.404
PEAK 2
38.244
PEAK 3
37.077
32.372
16.528
2.737
5.284
7.332

FIG._3B

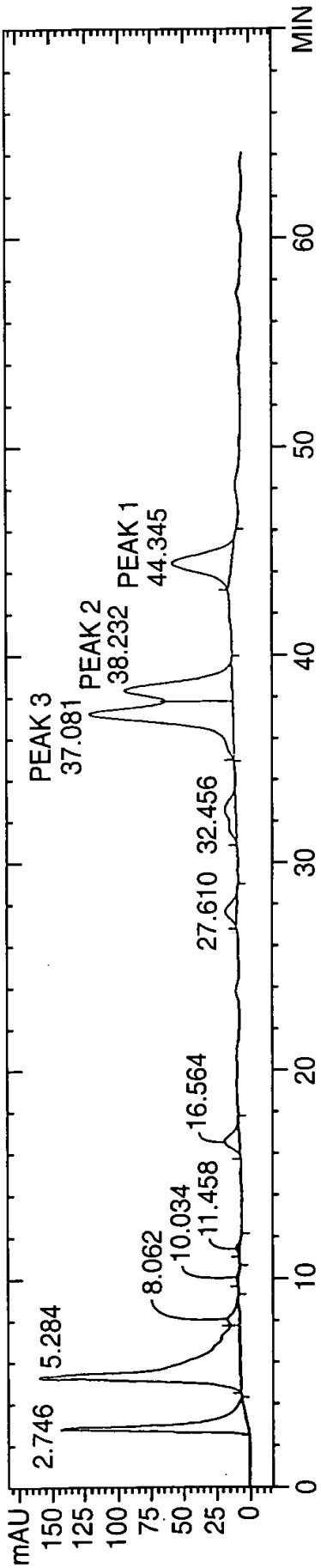
MIN
0
10
20
30
40
50
60
mAU
0
25
50
75
100
125
150
2.746
5.284
8.062
10.034
11.458
16.564
27.610
32.456
PEAK 3
37.081
PEAK 2
38.232
PEAK 1
44.345

FIG._3C

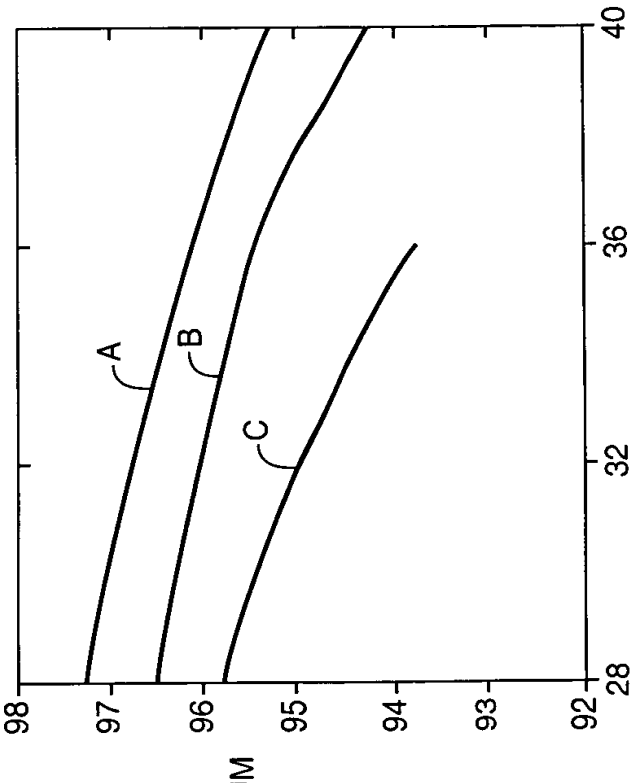
PERCENT MAXIMUM
GLUCOSE YIELD
98
97
96
95
94
93
92
40
36
32
28
A
B
C

FIG._6

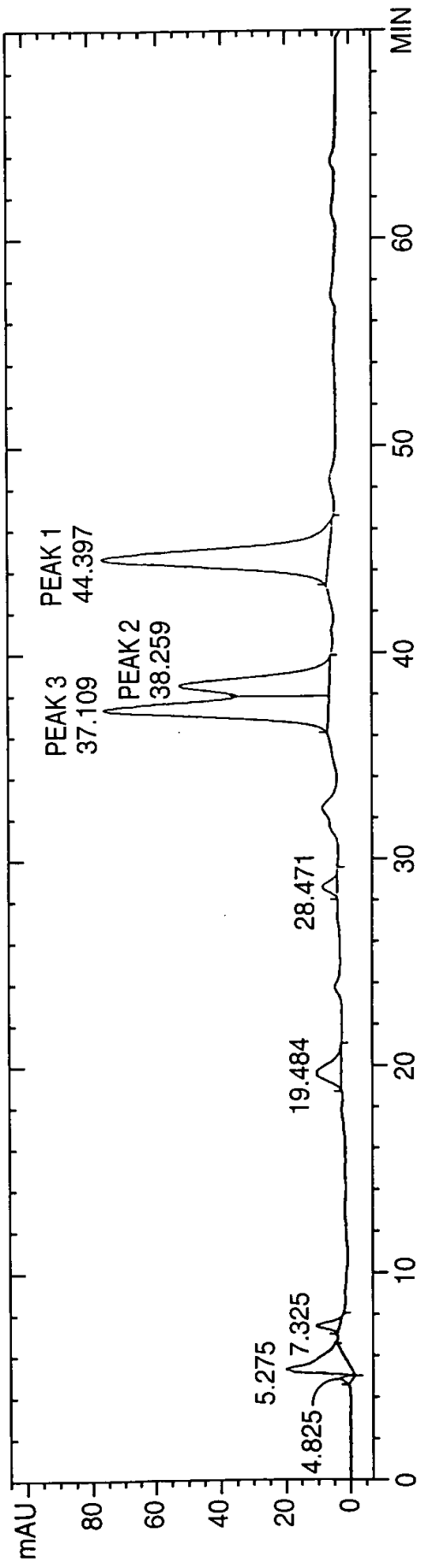
mAU
0
20
40
60
80
0
10
20
30
40
50
60
MIN
PEAK 1
44.397
PEAK 2
38.259
PEAK 3
37.109
28.471
19.484
7.325
5.275
4.825

FIG._4A

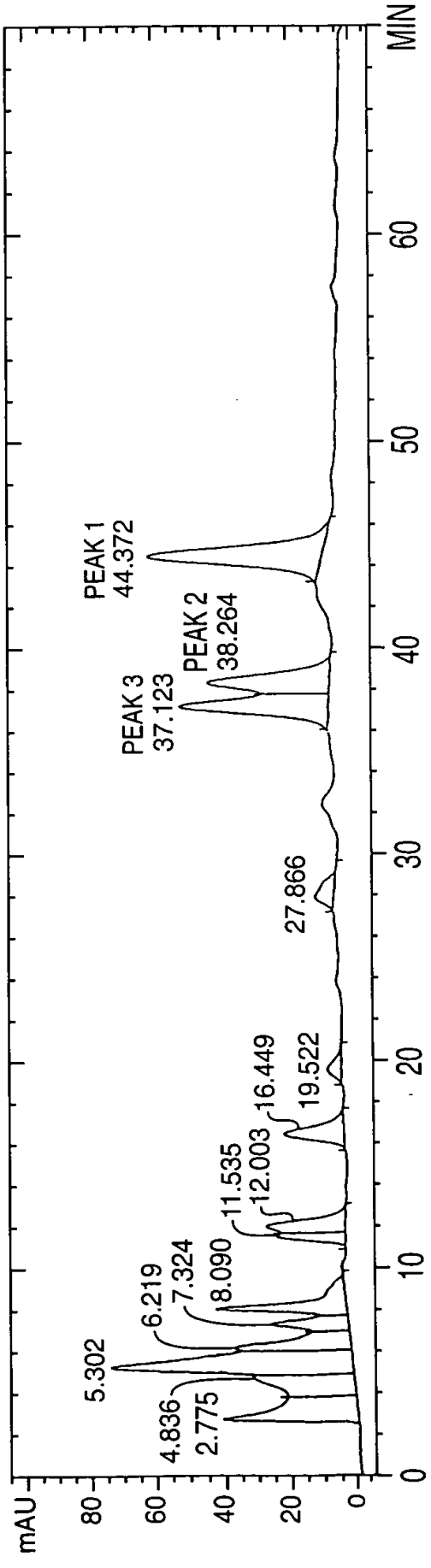
mAU
0
20
40
60
80
0
10
20
30
40
50
60
MIN
PEAK 1
44.372
PEAK 2
38.264
PEAK 3
37.123
27.866
19.522
16.449
12.003
11.535
8.090
7.324
6.219
5.302
4.836
2.775

FIG._4B

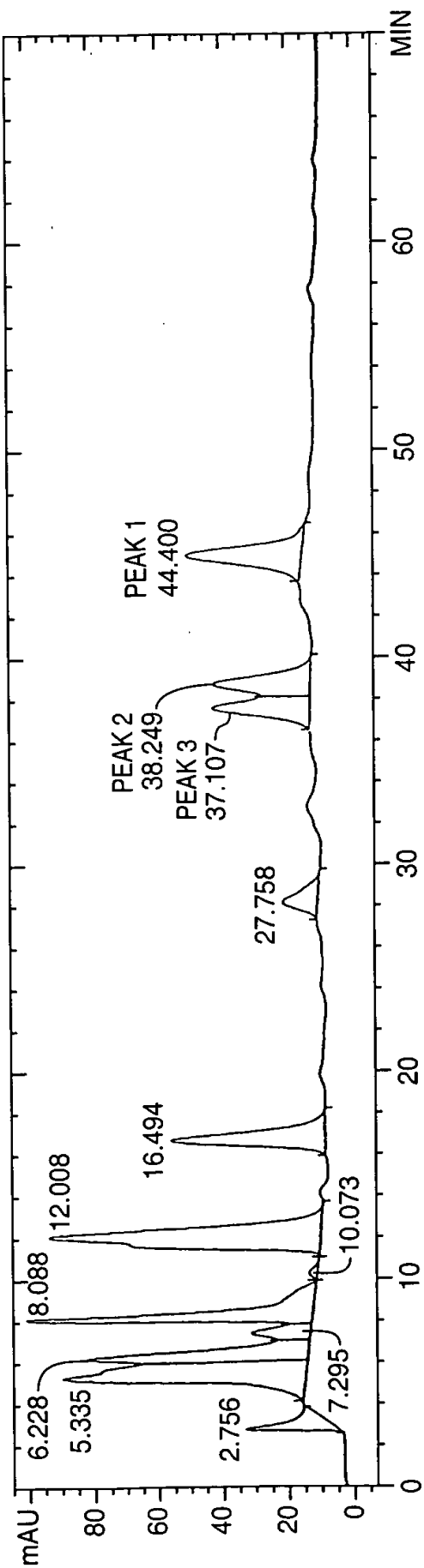
mAU
MIN
PEAK 1
44.400
PEAK 2
38.249
PEAK 3
37.107
27.758
16.494
12.008
10.073
8.088
6.228
5.335
2.756
7.295

FIG._4C

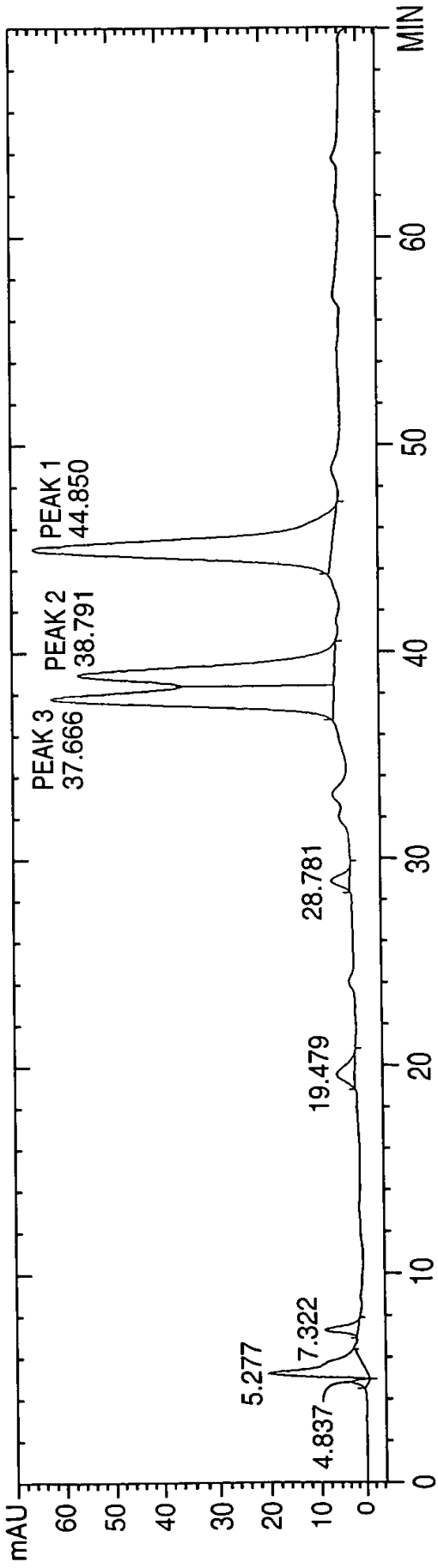
mAU
MIN
PEAK 1
44.850
PEAK 2
38.791
PEAK 3
37.666
28.781
19.479
7.322
5.277
4.837

FIG._4D

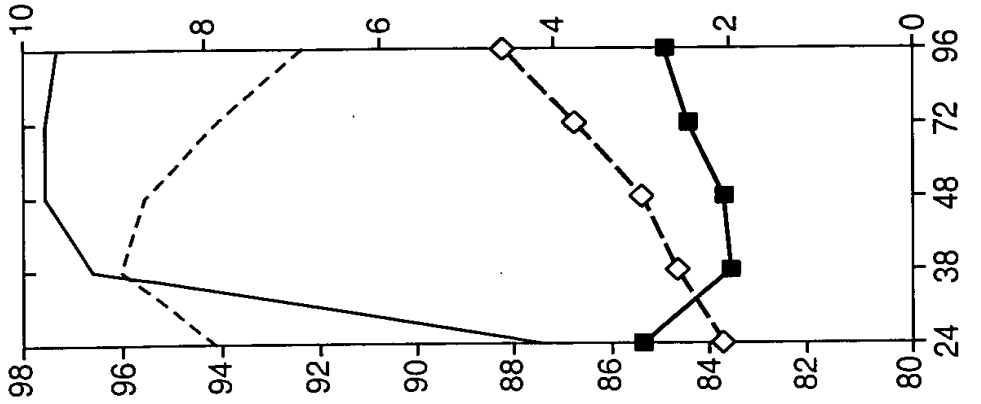

FIG._5C

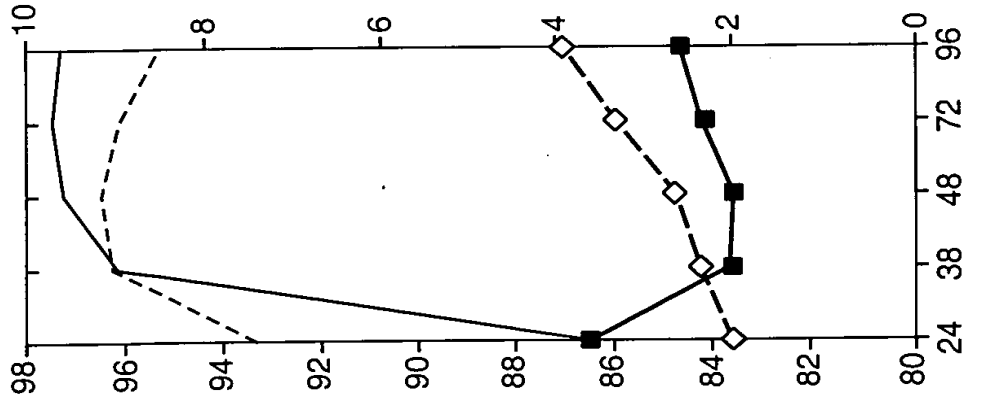

FIG._5B

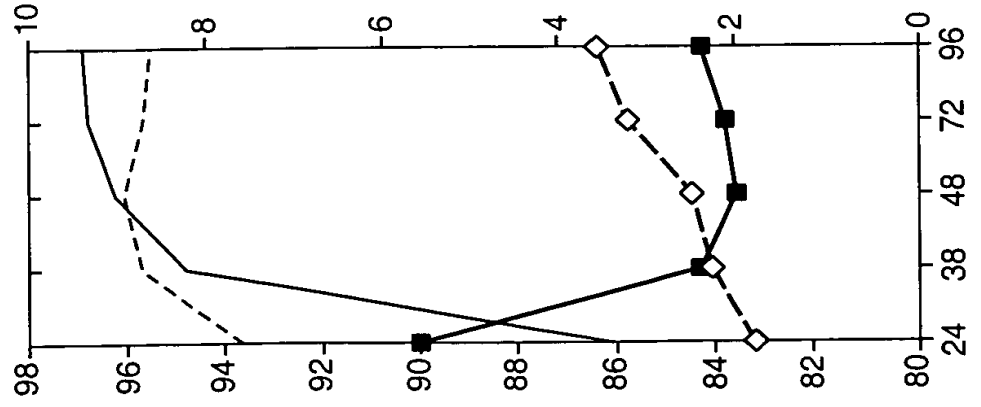

FIG._5A